### Instituto de Biología Funcional y Genómica

## Programa de Seminarios Externos "Dionisio Martín Zanca"

2023 - 2024

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## Pangenomes and their influence on bacterial phenotypes and evolution

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## **Abstract**

Understanding how variations in genotype translate to variation in phenotype is a long-standing problem in genetics. We are interested in improving our ability to predict the phenotypic consequences of genetic variants in bacteria; this is a difficult problem in the context of highly diverse bacterial genomes, with any pair of E. coli strains differing by ~30% of their gene content on average. I will present our computational and experimental work on understanding how this large genetic variability influences a range of important phenotypes such as pathogenicity, virulence, antimicrobial resistance and the rate of adaptation. We do this by developing computational methods tailored to the complexity of microbial pangenomes, applying them on datasets of bacterial clinical isolates, and running high-throughput laboratory evolution assays. Lastly, I will discuss the potential of the growing corpus of pathogen sequencing to develop real-time surveillance systems and train predictive models.



